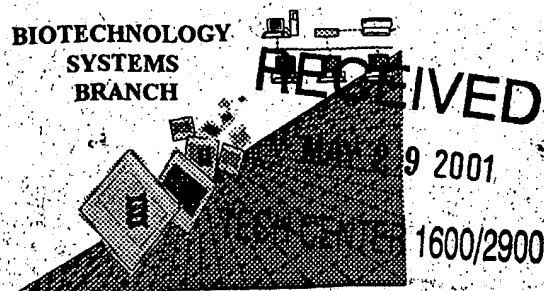


RAW SEQUENCE LISTING ERROR REPORT



The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/730,559A

Source: 1645

Date Processed by STIC: 5/11/2001

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or;
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW.

Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 - 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:

<http://www.uspto.gov/web/offices/pac/checker>

FSI
↓

Raw Sequence Listing Error Summary

ERROR DETECTED SUGGESTED CORRECTION

SERIAL NUMBER: 09/730,559A

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 Wrapped Nucleics The number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".

- 2 Wrapped Aminos The amino acid number/text at the end of each line "wrapped " down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".

- 3 Incorrect Line Length The rules require that a line not exceed 72 characters in length. This includes spaces.

- 4 Misaligned Amino Acid The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs
Numbering between the numbering. It is recommended to delete any tabs and use spacing between the numbers.

- 5 Non-ASCII This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.
Please ensure your subsequent submission is saved in ASCII text so that it can be processed.

- 6 Variable Length Sequence(s) contain n's or Xaa's which represented more than one residue.
As per the rules, each n or Xaa can only represent a single residue.
Please present the maximum number of each residue having variable length and
indicate in the (ix) feature section that some may be missing.

- 7 PatentIn ver. 2.0 "bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid
sequence(s) . Normally, PatentIn would automatically generate this section from the
previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section
to the subsequent amino acid sequence. **This applies primarily to the mandatory <220>-<223>
sections for Artificial or Unknown sequences.**

- 8 Skipped Sequences Sequence(s) missing. If intentional, please use the following format for each skipped sequence:
(OLD RULES) **(2) INFORMATION FOR SEQ ID NO:X:**
 (i) **SEQUENCE CHARACTERISTICS:**(Do not insert any headings under "SEQUENCE CHARACTERISTICS")
 (xi) **SEQUENCE DESCRIPTION:SEQ ID NO:X:**
 This sequence is intentionally skipped

Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).

- 9 Skipped Sequences Sequence(s) missing. If intentional, please use the following format for each skipped sequence.
(NEW RULES) **<210> sequence id number**
 <400> sequence id number
 000

- 10 Use of n's or Xaa's Use of n's and/or Xaa's have been detected in the Sequence Listing.
(NEW RULES) Use of <220> to <223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

- 11 Use of "Artificial" Use of "Artificial" only as "<213> Organism" response is incomplete, per 1.823(b) of New Sequence Rules.
(NEW RULES) Valid response is Artificial Sequence.

- 12 Use of <220>Feature Sequence(s) are missing the <220>Feature and associated headings.
(NEW RULES) Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial Sequence" or "Unknown"
Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of new Rules)

- 13 PatentIn ver. 2.0 "bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted
file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing).
Instead, please use "File Manager" or any other means to copy file to floppy disk.

1645

RAW SEQUENCE LISTING
 PATENT APPLICATION: US/09/730,559A

DATE: 05/11/2001
 TIME: 13:58:07

Input Set : A:\766.21 CIP sequence.txt
 Output Set: N:\CRF3\05112001\I730559A.raw

Does Not Comply
 Corrected Diskette Needed

4 <110> APPLICANT: ISHIWATA, TETSUYOSHI
 W--> 5 ~~<110>~~ APPLICANT: SAKURADA, MIKIKO
 W--> 6 ~~<110>~~ APPLICANT: KAWABATA, AYAKO
 W--> 7 ~~<110>~~ APPLICANT: NAKAGAWA, SATOSHI
 W--> 8 ~~<110>~~ APPLICANT: NISHI, TATSUNARI
 W--> 9 ~~<110>~~ APPLICANT: KUGA, TETSURO
 W--> 10 ~~<110>~~ APPLICANT: SAWADA, SHIGEMASA
 W--> 11 ~~<110>~~ APPLICANT: TAKEI, MASAMI
 W--> 12 ~~<110>~~ APPLICANT: SHIBATA, KENJI
 W--> 13 ~~<110>~~ APPLICANT: FURUYA, AKIKO
 15 <120> TITLE OF INVENTION: IgA NEPHROPATHY-ASSOCIATED GENE
 17 <130> FILE REFERENCE: 766.21 CIP
 19 <140> CURRENT APPLICATION NUMBER: US 09/730,559A
 20 <141> CURRENT FILING DATE: 2000-12-07
 22 <160> NUMBER OF SEQ ID NOS: 121
 24 <170> SOFTWARE: PatentIn Ver. 2.0

ppr 1-2
show <110> only ONCE - do not repeat for each applicant

ERRORED SEQUENCES

1488 <210> SEQ ID NO: 32
 1489 <211> LENGTH: 298
 1490 <212> TYPE: DNA
 1491 <213> ORGANISM: Homo sapiens
 1493 <400> SEQUENCE: 32
 E--> 1494 gcttatgatt acaaacatcc ctcatatgaa aatctcagca ttttctggct gctgccttca . 60
 1497 atogcttttt ctgaaatagg tatcccttga tgtcgactat ttgatttcag ccagtcggtt 120
 1500 ctctctggca gtgtccctg caaatgtgtc cttcaagaa aacaaaacct gcaagtggct 180
 1503 tgtaatgtac catgacctta tcatgtgaag gacaaatggc tcttgtgctt attagatagc 240
 1506 agatgaactg atgaactgaa ttcttgggtc gaagcttga taaggtcaga tgtctttg 298
 1817 <210> SEQ ID NO: 41
 1818 <211> LENGTH: 305
 1819 <212> TYPE: DNA
 1820 <213> ORGANISM: Homo sapiens
 1822 <400> SEQUENCE: 41
 E--> 1823 tcatgaagtg aagccaactg tttagactag aatgttatga gattaaacc accnnnnntt 60
 1826 attcatagac ataaacctc attttaatta gtggatctgg atttttgtca tatgtggaat 120
 1829 cataatttaa acaaatcaa ctaagatgat ccaagttcca cacaactgca cttcaatatt 180
 1832 caagtcggtg tgaagatgcc tgactactgc gtcacaagat tctgagctgt cgtaaaaagc 240
 1835 ctggctcggt gtttctatct atagtgtaca catgttgggt tataatcaca aacctggaac 300
 1838 tctgt 305
 1864 <210> SEQ ID NO: 43
 1865 <211> LENGTH: 244
 1866 <212> TYPE: DNA
 1867 <213> ORGANISM: Homo sapiens
 1869 <400> SEQUENCE: 43
 1870 tactcttcaa ccatgatttt tctctgatgg cctgtgtgaa cagattaatg gtgtccatct 60

see item 10 on Error Summary Sheet

see item 10

next page

RAW SEQUENCE LISTING

DATE: 05/11/2001

PATENT APPLICATION: US/09/730,559A

TIME: 13:58:07

Input Set : A:\766.21 CIP sequence.txt

Output Set: N:\CRF3\05112001\I730559A.raw

```

1873 aattccttcc ccactggggg aaagcaaata atcaggccca ttgcaaaaac tgctcttggt 120
1876 tgagcttcct gccttaaatc ataccacag tgaatggcgt ccctttatca ccgctaata 180
E--> 1879 ctctgacatc tctctccact cacatgtgag cctcctcagc tctcgaaaaa caagtcgtc 240
1882 tcgg 244
1886 <210> SEQ ID NO: 44
1887 <211> LENGTH: 258
1888 <212> TYPE: DNA
1889 <213> ORGANISM: Homo sapiens
1891 <400> SEQUENCE: 44
E--> 1892 tctcagaaaa ctccagatca aatgagatga gtatgggtgnn nagggctggc aattagagga 60
1895 tactctccaa tggatgatgaa gggagatgac tgggggaaat ccagcaggat gttgatttag 120
1898 tatgtacaca gtgagaggat acttgtagag aacctagaat cttctctgaa tgtgacgggc 180
1901 cctcagagat aattgttaac agataagtgg atgattaaat acatttcctc cagtaggcta 240
1904 gatgttaaga cggagatc 258

```

Handwritten notes:
 - Next to line 1879: *Item 10*
 - Next to line 1892: *Item 10*
 - Next to line 1892: *fyI*

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

VERIFICATION SUMMARY

DATE: 05/11/2001

PATENT APPLICATION: US/09/730,559A

TIME: 13:58:09

Input Set : A:\766.21 CIP sequence.txt

Output Set: N:\CRF3\05112001\I730559A.raw

L:5 M:280 W: Numeric Identifier already exists, <110> found multiple times
L:6 M:280 W: Numeric Identifier already exists, <110> found multiple times
L:7 M:280 W: Numeric Identifier already exists, <110> found multiple times
L:8 M:280 W: Numeric Identifier already exists, <110> found multiple times
L:9 M:280 W: Numeric Identifier already exists, <110> found multiple times
L:10 M:280 W: Numeric Identifier already exists, <110> found multiple times
L:11 M:280 W: Numeric Identifier already exists, <110> found multiple times
L:12 M:280 W: Numeric Identifier already exists, <110> found multiple times
L:13 M:280 W: Numeric Identifier already exists, <110> found multiple times
L:1047 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9
L:1150 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:14
L:1153 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:14
L:1494 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:32
L:1823 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:41
L:1879 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:43
L:1892 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:44
L:2828 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:115
L:2843 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:116
L:2897 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:120